

09/701618

529 Rec'd PCT/PTC 01 DEC 2000

SEQUENCE PROTOCOL

(1) GENERAL INDICATIONS:

(i) APPLICANT:

- (A) NAME: Deutsches Krebsforschungszentrum
- (B) STREET: Im Neuenheimer Feld 280
- (C) TOWN: Heidelberg
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 69120

(ii) TITLE OF THE INVENTION: Method for Triggering Apoptosis in Cells

(iii) NUMBER OF SEQUENCES: 10

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, version #1.30 (EPO)

(v) DATA OF THE CURRENT APPLICATION: not yet known

(vi) DATA OF THE PRIOR APPLICATION:

APPLICATION NUMBER: DE 198 24 811.3  
FILING DATE: June 3, 1998

(2) INDICATIONS AS TO ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1156 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(ix) CHARACTERISTIC:

- (A) NAME/KEY: CDS
- (B) POSITION: 118..540

(ix) CHARACTERISTIC:

- (A) NAME/KEY: mat\_peptide
- (B) Position: 118..540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTTTCCGGGA GACTGGAGTC GAAGGCCGTG AGTATTTCT AAGCCAGTGT TTAGAGAGTA	60
TGTGAGGCAA GAGTACCTAT AGAACCCGGA GGAGGGTGAG GAGCAGAGCT GGCCATA	117
ATG GCA GGT GAA GAA ATT AAT GAA GAC TAT CCA GTA GAA ATT CAC GAG Met Ala Gly Glu Glu Ile Asn Glu Asp Tyr Pro Val Glu Ile His Glu	165
1 5 10 15	
TAT TTG TCA GCG TTT GAG AAT TCC ATT GGT GCT GTG GAT GAG ATG CTG Tyr Leu Ser Ala Phe Glu Asn Ser Ile Gly Ala Val Asp Glu Met Leu	213
20 25 30	
AAG ACC ATG ATG TCT TCT AGA AAT GAG TTG TTG CAG AAG TTG GAT Lys Thr Met Met Ser Val Ser Arg Asn Glu Leu Leu Gln Lys Leu Asp	261
35 40 45	
CCA CTT GAA CAA GCA AAA GTG GAT TTG GTT TCT GCA TAC ACA TTA AAT Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser Ala Tyr Thr Leu Asn	309
50 55 60	
TCA ATG TTT TGG GTT TAT TTG GCA ACC CAA GGA GTT AAT CCT AAG GAA Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly Val Asn Pro Lys Glu	357
65 70 75 80	
CAT CCA GTA AAA CAG GAA TTG GAA AGA ATC AGA GTA TAT ATG AAC AGA His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg Val Tyr Met Asn Arg	405
85 90 95	
GTC AAG GAA ATA ACA GAC AAG AAA AAG GCT GGC AAG CTG GAC AGA GGT Val Lys Glu Ile Thr Asp Lys Lys Ala Gly Lys Leu Asp Arg Gly	453
100 105 110	
GCA GCT TCA AGA TTT GTA AAA AAT GCC CTC TGG GAA CCA AAA TCG AAA Ala Ala Ser Arg Phe Val Lys Asn Ala Leu Trp Glu Pro Lys Ser Lys	501
115 120 125	
AAT GCA TCA AAA GTT GCC AAT AAA GGA AAA AGT AAA AGT TAACTTTTG Asn Ala Ser Lys Val Ala Asn Lys Gly Lys Ser Lys Ser	550
130 135 140	
GTCCCCATGATGT ACACATATTC AAAAAGTACA TTAATATGTA ATCACAGTAA TATGTAAAGC	610
TAAATACATTCT CTCTCCAAAG ATCATTATCT TTATTGATTA GCACTGAGGA TTTAACATT	670
GTGATATATT ATATATTAT AATTTACCAT CTCTTGATGA GACTCTTATT TCTTTATATA	730
GGTCAGTCTT GCAAGTACCA TTTTATAAGC AGCTGTGAAA TTTAAGTGAA ATGTTCTTG	790
TAAACATTTG TACTATTTA AATGAATAAT GACCTTATGA AGTATGCTAT CTGTAGGCTG	850
AAATTATAGG TACATCTGTT TTCACTATAT GATATTAAGA AAGCGTGAAT GACTTAAATG	910
TTCATTTTT TCTGTATAGA TACTTTATCA TGTTTCATG ATTTTAGGAA TTACTGCTTT	970

GTTGATATTCAAAAGTGTGAA	ACTAAAAGTTTATGGTTGTA	CTTTAATTCTCTGCATGTTG	1030
CCTCTATGTC CCATTTAAAAA	TAAAATACAT TCTCATTAAAC	TTTAGATGGG AAATAAGGTT	1090
GTATGTTGAT GGATGAATT	TGGCATGATG ACTGTACTCT	CAATAAAAGGC TGAAAATGTT	1150
GTAAAAA			1156

## (2) INDICATIONS AS TO ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 141 amino acids
  - (B) KIND: amino acid
  - (D) TOPOLOGY: linear

- (ii) KIND OF MOLECULE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

Met	Ala	Gly	Glu	Glu	Ile	Asn	Glu	Asp	Tyr	Pro	Val	Glu	Ile	His	Glu
1					5					10			15		
Tyr	Leu	Ser	Ala	Phe	Glu	Asn	Ser	Ile	Gly	Ala	Val	Asp	Glu	Met	Leu
							20		25				30		
Lys	Thr	Met	Met	Ser	Val	Ser	Arg	Asn	Glu	Leu	Leu	Gln	Lys	Leu	Asp
						35		40				45			
Pro	Leu	Glu	Gln	Ala	Lys	Val	Asp	Leu	Val	Ser	Ala	Tyr	Thr	Leu	Asn
						50		55			60				
Ser	Met	Phe	Trp	Val	Tyr	Leu	Ala	Thr	Gln	Gly	Val	Asn	Pro	Lys	Glu
						65		70		75			80		
His	Pro	Val	Lys	Gln	Glu	Leu	Glu	Arg	Ile	Arg	Val	Tyr	Met	Asn	Arg
						85			90			95			
Val	Lys	Glu	Ile	Thr	Asp	Lys	Lys	Ala	Gly	Lys	Leu	Asp	Arg	Gly	
						100			105			110			
Ala	Ala	Ser	Arg	Phe	Val	Lys	Asn	Ala	Leu	Trp	Glu	Pro	Lys	Ser	Lys
						115			120			125			
Asn	Ala	Ser	Lys	Val	Ala	Asn	Lys	Gly	Lys	Ser	Lys	Ser			
						130			135			140			

## (2) INDICATIONS AS TO ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 1040 base pairs
  - (B) KIND: nucleotide
  - (C) STRAND FORM: single strand
  - (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(ix) CHARACTERISTIC:

  - (A) NAME/KEY: CDS
  - (B) POSITION: 78..500

(ix) CHARACTERISTIC:

  - (A) NAME/KEY: mat\_peptide
  - (B) Position: 78..500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAAGCCGT GTCATGGCGT CATCATCGTG CGACCTATTG CCCGGAGACA GGC GTCCACG	60
STATTGAGTT GGT CACA ATG GCA GGT GAA GAA ATG AAT GAA GAT TAT CCC	110
Met Ala Gly Glu Met Asn Glu Asp Tyr Pro	
1 5 10	
STA GAA ATT CAC GAG TCT TTA ACA GCC CTG GAG AGC TCC CTG GGT GCT	158
Val Glu Ile His Glu Ser Leu Thr Ala Leu Glu Ser Ser Leu Gly Ala	
15 20 25	
CTG GAC GAC ATG CTG AAG ACC ATG ATG GCT GTT TCT AGA AAC GAG TTG	206
Val Asp Asp Met Leu Lys Thr Met Met Ala Val Ser Arg Asn Glu Leu	
30 35 40	
TG CAG AAG TTG GAC CCA TTG GAA CAA GCA AAG GTG GAT TTA GTT TCT	254
Leu Gln Lys Leu Asp Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser	
45 50 55	
GCA TAC ACC TTA AAT TCA ATG TTT TGG GTT TAT TTG GCA ACT CAA GGA	302
Ala Tyr Thr Leu Asn Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly	
60 65 70 75	
TTT AAT CCC AAA GAG CAT CCA GTG AAG CAG GAA CTG GAA AGA ATC AGA	350
Val Asn Pro Lys Glu His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg	
80 85 90	
TCT TAC ATG AAC AGA GTT AAA GAA ATA ACA GAC AAG AAG AAG GCT GCC	398
Val Tyr Met Asn Arg Val Lys Glu Ile Thr Asp Lys Lys Lys Ala Ala	
95 100 105	
AG CTG GAC AGA GGT GCT GCT TCG AGA TTT GTC AAG AAG GCA CTC TGG	
446	

Lys Leu Asp Arg Gly Ala Ala Ser Arg Phe Val Lys Lys Ala Leu Trp			
110	115	120	
GAA CCC AAA CGA AAA AGC ACA CCA AAA GTG GCT AAT AAA GGG AAA AGC			494
Glu Pro Lys Arg Lys Ser Thr Pro Lys Val Ala Asn Lys Gly Lys Ser			
125	130	135	
AAA CAC TAATCTTTG GTTTGATGT ACATGTTTC AAAAGTACA TCCTTTAA			550
Lys His			
140			
TCAGTTACA ATGTAGTTAT GTGACCATGT GGTGTTAAA TGGATTCCCT TTGGAATTCA			610
TGTATAAATT TACACATTAC ATTTGTGATA CTGAATCTT TTTTGCTGA GAAAGATTAA			670
GTTGCTTTG TTGATTTCA TATAAAGCAT CATGATGTGT TTAATATTGT AAGATATTCT			730
ATAAGCAGTT GTGAAATCCA AATGTTCTCT GTAAACATTT GTAGTGTGAAATGAACAA			790
TGATATTATG AAGTGTGCTA TCTGTAGACC TCGAGGTGTA AGGACATTTG TTTTCAGTAA			850
TGATGAGAAA TACAGTGACT TAAATACCCA CTCTGTTCT GTTCAGTTAG TTCAACATGT			910
TTCGTGATTT TTTTTTTTT TTGAGTAATT CTGCTTGAT ATTCAAAGTC AAAATTGAAA			970
CCTTAAGGCT GTACTTAAT TCCTCATGTT CCATTTAAAA TAAAATGTT TCATTAACTC			1030
TGATGGAAAA			1040

## (2) INDICATIONS AS TO ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 141 amino acids
  - (B) KIND: amino acid
  - (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ala Gly Glu Glu Met Asn Glu Asp Tyr Pro Val Glu Ile His Glu			
1	5	10	15
Ser Leu Thr Ala Leu Glu Ser Ser Leu Gly Ala Val Asp Asp Met Leu			
20	25	30	
Lys Thr Met Met Ala Val Ser Arg Asn Glu Leu Leu Gln Lys Leu Asp			
35	40	45	
Pro Leu Glu Gln Ala Lys Val Asp Leu Val Ser Ala Tyr Thr Leu Asn			
50	55	60	
Ser Met Phe Trp Val Tyr Leu Ala Thr Gln Gly Val Asn Pro Lys Glu			

65	70	75	80
His Pro Val Lys Gln Glu Leu Glu Arg Ile Arg Val Tyr Met Asn Arg			
85	90	95	
Val Lys Glu Ile Thr Asp Lys Lys Ala Ala Lys Leu Asp Arg Gly			
100	105	110	
Ala Ala Ser Arg Phe Val Lys Lys Ala Leu Trp Glu Pro Lys Arg Lys			
115	120	125	
Ser Thr Pro Lys Val Ala Asn Lys Gly Lys Ser Lys His			
130	135	140	

(2) INDICATIONS AS TO ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) KIND: nucleotide
  - (C) STRAND FORM: single strand
  - (D) TOPOLOGY: linear
  
- (ii) KIND OF MOLECULE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"
  
- (iii) HYPOTHETICAL: no
  
- (iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGGTACCAT GGCAGGTGAA GAAATTAATG AAGACTAT

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(2) INDICATIONS AS TO ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) KIND: nucleotide
  - (C) STRAND FORM: single strand
  - (D) TOPOLOGY: linear
  
- (ii) KIND OF MOLECULE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"
  
- (iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGGTCGACTT AACTTTACT TTTTCCTTTA TTGGCAAC

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(2) INDICATIONS AS TO ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGGGTACCAT GGCAGGTGAA GAAATGAATG AAGATTAT

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(2) INDICATIONS AS TO ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) KIND: nucleotide
- (C) STRAND FORM: single strand
- (D) TOPOLOGY: linear

(ii) KIND OF MOLECULE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGTCGACGT GTTGCTTT CCCTTATTA GCCACTTT

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